19. (Twice Amended) A method of identifying an agent which modulates expression of a gene which is modulated by a filamentation MAPK pathway in a fungus, comprising the steps of:

a) transforming a suitable host cell with an expression vector comprising a nucleic acid molecule encoding a gene selected from the group consisting of: PGU1, FLO11, TOT10/YEL033W, SRD1, TOT12/YKR105C, TOT13/YOR225W, FLO5, DDR48, TOT11/YLR042C, TOT7/YER158C, TOT8/YIL117C, TOT20/YHL049C, TOT15/YLR434C, TOT14/YBR113W, TOT9/YIR013C, PHO84, KTR2, and SJH1;

b) contacting said host cell with an agent to be tested; and

c) comparing the expression of said gene in the presence of the agent with the expression of said gene in the absence of said agent, wherein a difference in the expression of said gene in the presence of the agent as compared with in the absence of the agent indicates that the agent modulates expression of said gene which is modulated by the filamentation MAPK pathway in a fungus.

Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (pages vi - viii).

REMARKS

Amendments to the Specification and Renumbering of the Figures

The Specification has been amended to correct minor grammatical errors and to incorporate the information contained in originally-filed Figure 1. Figures 1 and 4 have been removed, and the remaining figures have been appropriately renumbered.

No new matter has been added.

Amendments to the Claims

Claims 9, 15 and 19 have been amended for clarification purposes only. Support for these amendments can be found throughout the Specification, for example at page 8, lines 21-24, page 9, lines 13-22 and page 10, lines 5-13.

No new matter has been added.

Formal Drawings

Submitted concurrently are re-numbered Formal Figures 1-4, 5A-C, 6-8 and-9A-B. As noted above, originally filed Figures 1 and 4 have been removed and the information contained therein has been incorporated into the Specification.

Rejection of Claims 9, 11, 15 and 19 Under 35 U.S.C. § 112, first paragraph

Claims 9, 11, 15 and 19 are rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Each point raised by the Examiner is discussed below.

A. The Examiner states that "[a] critical element of applicants' invention is the presence of regulatory sequences for each of the recited *genes* that are responsive to modulation of the MAPK filamentous pathway of yeast" (Office Action, page 3, emphasis in original).

Applicants respectfully disagree that the regulatory sequences of the claimed genes are required to practice the invention. The present invention is directed, *inter alia*, to methods of identifying agents that modulate the expression of genes as provided in the application as filed. The modulation of gene expression can be mediated by a variety of mechanisms, as will be appreciated by one of skill in the art. For example, anti-sense oligonucleotides can inhibit gene expression by binding, for example, to the ATG start site of the target gene. Alternatively, ribozymes can be used to catalyze site-specific cleavage of mRNAs encoded by a target gene and, thus, inhibit gene expression. Other agents which can inhibit expression of a gene include agents that target the protein encoded by the gene of interest to the ubiquitination pathway, thereby targeting the protein for degradation and, thus, inhibiting its expression and activity.

Thus, one of ordinary skill in the art can envisage multiple ways to inhibit gene expression without necessarily requiring MAPK-responsive regulatory sequences.

Additionally, methods of enhancing gene expression are also known to one of ordinary skill in the art. Agents that can mediate such a response include those that enhance the stability of an mRNA, or alternatively promote mRNA translation, or stabilize the protein encoded by the target gene, such as heat shock proteins or chaperones. Such agents can act to enhance gene expression without the need for MAPK-responsive regulatory elements.

The Examiner also states that "[i]t is not at all clear that the information provided by the cited web site would have taught one of skill in the art the necessary regulatory sequences required to practice the claimed invention (i.e. MAPK-responsive regulatory sequences)" (Office Action, page 3).

Applicants respectfully disagree. Notwithstanding the fact that MAPK-responsive regulatory sequences are not required as discussed above, the yeast genome was fully sequenced and made publicly available in 1996 (see Exhibit 1). Thus, at the time the application was filed, one of skill in the art could identify the regulatory elements for the genes disclosed in the present application utilizing routine experimentation. The location of the genes, as claimed, could readily be identified in the sequenced genome, and the 5' regulatory sequences could as easily be located.

The eighteen genes, as disclosed, can be identified in the yeast genome by their systematic gene name, such that the name itself imparts specific information about the gene location in the yeast genome (see Exhibit 2). Specifically, the first letter of the yeast systematic name in, for example, YEL033W, denotes "yeast"; the second letter (in this example, "E"), denotes the chromosome number (i.e., 5); the third letter denotes which chromosome arm (L for left); the number denotes the open reading frame as numbered sequentially from the centromere to the telomere (in this example, the 33rd ORF); and the final letter denotes the location of the gene on either the Watson or Crick strand (in this example, the Watson strand). Clearly one of skill in the art would be able to locate the genes as disclosed, along with their regulatory sequences. Furthermore, the screening of such regulatory sequences can be performed by one of ordinary skill in the art using Applicants' specification as filed and routine techniques. For example, it would be routine for one of ordinary skill in the art to make a promoter-*lacZ* fusion comprising the regulatory sequence retrieved from the database and perform β-galactosidase

assays to assess the level of gene expression generated by the promoter-*lacZ* fusion. β-galactosidase assays provide a reliable method to verify the level of gene expression directed by the regulatory regions.

This approach is exemplified by Madhani *et al.* (*Proc. Nat. Acad. Sci.* 96:12530-12535 (1999)) (cited by the Examiner in paper number 4). Madhani *et al.* teach that "[t]he intergenic upstream region of *PGU1* was amplified and placed upstream of the *Escherichia coli lacZ* gene on the *URA3*-marked high-copy yeast shuttle plasmid YEp356R (9) by using the BamHI site, yielding a *PGU1* promoter-*lacZ* fusion" (Madhani *et al.* page 12531, first column, fourth paragraph). Madhani *et al.* also teach that "[c]onsistent with the *PGU1* transcript profile, a *PGU1-lacZ* promoter fusion gene depends on the MAPK pathway for its activity (Fig 3A)" (Madhani *et al.* page 12532) and that "[t]he filamentation MAPK pathway controls the *PGU1* promoter" (Madhani *et al.* page 12533, Fig. 3 legend). Thus, Madhani *et al.* teach that the regulatory sequence of *PGU1* can be identified using routine methods.

B. The Examiner states that "one of the requirements for biological materials under 37 §§ C.F.R. 1.801-1.809 is that the material be readily available to the public. There is no guarantee that the cited web sites will be available to the public for the entire term that would be granted upon issuance of a patent on the instant claims" (Office Action, page 3).

Applicants respectfully disagree. The M.P.E.P. (8th ed., February 2003 Revision) at section 2404.01 states that:

> "If the biological material and its natural location can be adequately described so that one skilled in the art could obtain it using ordinary skill in the art, the disclosure would appear to be sufficient to meet the enablement requirement of 35 U.S.C. 112 without a deposit so long as its degree of availability is reasonable under the circumstances."

Applicants submit that *Saccharomyces cerevisiae* is a common laboratory organism, widely available and commonly used. Furthermore, the identification and isolation of genetic sequences is standard practice for those of ordinary skill in the art using techniques, such as RT-PCR. Such techniques are standard and reliable methods, and, as such, the biological sequences described in the invention do not require a biological deposit in accordance with the M.P.E.P., 8th ed., February 2003 Revision § 2404.02.

Furthermore, the M.P.E.P. also states that:

> "Unless there is a reasonable basis to believe that the biological material will cease to be available during the enforceable life of the patent, current availability would satisfy the requirement. The incentives provided by the patent system should not be constrained by the mere possibility that a disclosure that was once enabling would become non-enabling over a period of time through no fault of the patentee" (M.P.E.P., 8th ed., February 2003 Revision, § 2404.01; citation omitted).

Applicants do not believe there is any reasonable basis to believe that *S. cerevisiae* will cease to exist, or that the information of the sequenced genome of *S. cerevisiae* will cease to exist during the enforceable life of this application if allowed and issued as a patent, and the Examiner has not presented evidence to the contrary. Nevertheless, should the biological material become unavailable, or the sequence information cease to exist, Applicants bear the risk that the patent is deemed invalid at that time (M.P.E.P., 8th ed., February 2003 Revision, § 2404.01).

C. The examiner has stated that "[w]ith regard to claim 19, it is not at all clear that the relevant coding and regulatory sequences were available to the public at the time of filing for each of the additional genes recited in the claim" (Office Action, page 4).

For the reasons already discussed above, Applicants respectfully disagree. Again, the regulatory sequences are not necessary to practice the invention. The yeast genome was sequenced in 1996 and the eighteen genes recited in Claim 19 were provided with their systematic name in the Specification as filed, for example in originally-filed Figure 1 (now incorporated into the text of the Specification). No biological deposit is required where the required biological materials can be obtained from publicly available material with only routine experimentation and a reliable screening test. (M.P.E.P. 8th ed., February 2003 Revision, § 2404.02). Thus, Applicants have provided an enabling disclosure such that one skilled in the art could make and/or use the invention. Reconsideration and withdrawal of the rejection are respectfully requested.

Rejection of Claim 19 Under 35 U.S.C. § 112, First Paragraph

Claim 19 is rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the Specification in such a way as to reasonable convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention (Office Action, page 4).

Again, the Examiner alleges that "a critical feature of applicants' invention is the presence of regulatory sequences." Applicants maintain that regulatory sequences are not necessary to practice Applicants' invention, as discussed *supra*, and even if utilized, such regulatory elements can be readily identified and obtained by one of skill in the art using techniques that are standard in the art together with Applicants' disclosure as filed.

The Examiner also states that "[t]he claims also encompass a potentially large genus of genes in that the claims are directed towards 'a filamentation MAPK pathway in a fungus.' Thus, a large number of potential genes (including MAPK responsive elements) from a large number of different fungi are encompassed by the rejected claim" (Office Action, pages 4-5).

Applicants respectfully disagree. The Examiner is using the preamble to increase the breadth of the claims. The M.P.E.P. (8th ed., February 2003 Revision) at § 2111.02, states that the preamble is not considered a limitation, if the preamble merely states the purpose or intent of the invention:

> If the body of the claim fully and intrinsically sets forth all the limitations of the claimed invention, and the preamble merely states, for example the purpose or intended use of the invention, rather than any distinct definition of any of the claimed invention's limitations, then the preamble is not considered a limitation and is of no significance to claim construction.

The preamble of Claim 19 merely states the purpose of the invention, which is to identify agents that modulate the MAPK pathway in a fungus. The body of Claim 19 clearly sets forth all limitations of the invention including the recitation of specific genes. Specifically, Claim 19, as amended, recites "A method of identifying an agent which modulates expression of a gene which is modulated by a filamentation MAPK pathway in a fungus, comprising the steps of: a) transforming a suitable host cell with an expression vector comprising a nucleic acid molecule encoding a gene selected from the group consisting of: PGU1, FLO11, TOT10/YEL033W, SRD1, TOT12/YKR105C, TOT13/YOR225W, FLO5, DDR48, TOT11/YLR042C, TOT7/YER158C, TOT8/YIL117C, TOT20/YHL049C, TOT15/YLR434C, TOT14/YBR113W, TOT9/YIR013C, PHO84, KTR2, and SJH1; b) contacting said host cell with an agent to be tested; and c) comparing the expression of said gene in the presence of the agent with the expression of said gene in the absence of said agent, wherein a difference in the expression of said gene in the presence of the agent as compared with in the absence of the agent indicates that

the agent modulates expression of said gene which is modulated by the filamentation MAPK pathway in a fungus." Thus, Claim 19 does not include a large number of potential genes, but instead encompasses a specific set of eighteen genes. Since the recited genes, with their disclosed systematic names, provided in the Specification as filed, adequately describes the claimed invention, Applicants were clearly in possession of the invention when the application was filed.

The Examiner also states that "[t]he cited passages from the specification provided in Paper No. 10 for support of the claimed method ... does not provide literal support for the claimed method" and "[t]hus, the amendment to include each of the recited genes is considered to be NEW MATTER" (Office Action, page 5).

Applicants respectfully disagree. Literal support for the claimed method is not required:

> While there is no *in haec verba* requirement, newly added claim limitations must be supported in the specification through express, implicit, or inherent disclosure (M.P.E.P., 8th ed., February 2003 Revision, § 2163).

In any event, further support for this amendment is also found in Figure 1 (as originally filed, now incorporated into the text of the Specification), which was entitled "Genetic Expression Profiles of 18 Genes Regulated by the Filamentation MAPK Pathway." Amending Claim 19 to recite the disclosed eighteen genes does not constitute new matter.

Furthermore, the Examiner states that "the specification does not provide any description of the genes recited in claim 19 other than a name" (Office Action, page 5).

As stated in the M.P.E.P. (8th ed., February 2003 Revision) at § 2163.02, the specification complies with the written description requirement if it conveys with reasonable clarity that the Applicants were in possession of the invention at the time of filing:

> The test for sufficiency of support in a parent application is whether the disclosure of the application relied upon 'reasonably conveys to the artisan that the inventor had possession at the time of the later claimed subject matter.'

As discussed above, the recitation of the gene name, and particularly of the systematic yeast name, imparts specific and descriptive characteristics of the genes in the claimed invention such that one of skill in the art could at once envisage Applicants' claimed invention at the time of filing of the application and thus would reasonably conclude that Applicants were in

possession of their claimed invention. Reconsideration and withdrawal of the rejection are respectfully requested.

Rejection of Claims 9, 11, 15 and 19 Under 35 U.S.C. § 112, Second Paragraph

Claims 9, 11, 15 and 19 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. Specifically, the Examiner states that the "claims are vague and indefinite in that there is no explicit linkage of the nucleic acid to be expressed (*i.e.*, a gene) with the recited gene (*e.g.*, PGU1, etc.)."

Claims 9, 15 and 19 have been amended to address this issue. Claim 11 depends from Claim 9. Reconsideration and withdrawal of the rejection are respectfully requested.

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (978) 341-0036.

Respectfully submitted,

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MARKED UP VERSION OF AMENDMENTS

Specification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace the paragraph at page 3, line 28 through page 4, line 8 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Compounds or molecules which activate or inhibit PGUI can also be identified. For example, activators of this pectinase can be identified by expressing PGUI in an appropriate host cell (e.g., a bacterial or yeast cell), contacting the cells with (e.g., by culturing them in the presence of) candidate activators (compounds or molecules to be assessed for their effects on PGUI activity) and determining their effect on PGUI (e.g., whether they enhance or activate PGUI expression or activity, repress or decrease PGUI expression or activity or have no effect). Compounds which enhance or activate [PHUI] PGUI expression or activity are activators; those which repress or decrease its expression or activity are inhibitors). Activators and inhibitors of PGUI are also the subject of this invention.

Replace the paragraph at page 4, lines 9 through 24 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Also the subject of this invention is a method of inhibiting (totally or partially) invasion of a host, particularly a plant host by a fungus (i.e., a method of inhibiting fungal invasion of a host). In the method, a compound or molecule which inhibits the MAPK pathway or specifically inhibits [TOTI0/YELO33W] TOT10/YELO33W is applied to a host (e.g., by application to a plant surface) in such a manner that it contacts the fungus (e.g., the yeast) and inhibits one or more components of the MAPK pathway, such as TOT10/YELO33W. For example, an inhibitor can be a compound which binds and inhibits TOT10/YELO33W; galacturonic acid; or a mimic of galacturonic acid which represses TOT10/YELO33W. In a specific embodiment, the method of inhibiting fungal invasion of a host comprises contacting a fungus (e.g., a yeast) with a compound which inhibits the MAPK pathway and/or inhibits TOT10/YELO33W, in sufficient quantity that inhibition of the

MAPK pathway and/or inhibition of TOT10/YELO33W occurs, thereby inhibiting fungal invasion of the host. In a further embodiment, the host is a plant and the compound is applied to a plant surface (e.g., root, leaf, stem) or seed in such a manner that it contacts the fungus and inhibits (totally or partially) the ability of the fungus to invade.

Replace the paragraph at page 4 line 28 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [2] 1 lists MAPK pathway targets.

Replace the paragraph at page 5, line 1 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [3] 2 summarizes results of systematic knockout experiments.

Replace the paragraph at page 5, lines 4 through 5 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [5] 3 shows genes selectively induced by the plant-specific carbohydrate polygalacturonic acid and its hydrolysis product.

Replace the paragraph at page 5, lines 6 through 7 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [6] 4 shows genes selectively repressed by the plant-specific carbohydrate polygalacturonic acid and its hydrolysis product.

Replace the paragraph at page 5, line 8 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figures [7] 5A-C is a compilation of MAPK data, sorted as TEC1-high copy/tec1Δ.

Replace the paragraph at page 5, lines 9 through 10 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [8] 6 shows results of profiling experiments with polygalacturonic acid (PGA) and galacturonic acid (GA), sorted by PGA/YPD.

Replace the paragraph at page 5, lines 11 through 12 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [9] 7 shows results of profiling experiments with polygalacturonic acid (PGA) and galacturonic acid (GA), sorted by GA/YPD.

Replace the paragraph at page 5, lines 13 through 14 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure [10] 8 shows a flow chart of homologous genes induced by the filamentation and mating MAPK pathways.

Replace the paragraph at page 5, lines 15 through 16 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figures [11] 9A-B shows a listing of genes whose expression is reduced in STE12$^-$, STE7$^-$ but show greater than double an effect with Tec1.

Replace the paragraph at page 5, line 19 through page 6, line 2 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Described herein is work carried out to identify and study the targets of the MAP kinase pathway in order to understand how signaling cascades control a developmental switch in this *Saccharomyces cerevisiae* model system. The pathway consists of four kinases Ste20 (PAK), Ste11 (MEKK), Ste7 (MEK) and Kss1 (MAPK), which display both positive and negative control over the

pathway, as well as a heterodimeric transcription factor Tec1-STE12. STE7, STE11 and STE20 also participate in the yeast mating MAPK pathway. Global expression patterns in haploid cells under rich medium conditions were examined in the following mutants: wild type [tec1$_\Delta$] tec1Δ Ste12Δ, Ste7Δ, TEC1-overexpression, and STE11-4 (an activated mutant of the MEKK). Expression profiling was carried out using nucleic acid arrays (chips) such as described in WO95/11995. One chip set was used per sample (chips with obvious defects were redone).

Replace the paragraph at page 6, lines 3 through 11 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

18 genes were identified that show strong regulation by the pathway-specific transcription factor Tec1 (i.e. 3.5-20X difference in expression comparing TEC1-overexpression to tec1Δ). These 18 genes are as follows:

PGU1 (YJR153W)

FLO11 (YIR019C)

ORF (YEL033W)

SRD1 (YCR018C)

ORF (YKR105C)

ORF (YOR225W)

FLO5 (YHR211W)

DDR48 (YMR173W)

ORF (YLR042C)

ORF (YER158C)

ORF (YIL117C)

ORF (YHL049C; _f)

ORF (YLR434C)

ORF (YBR113W)

ORF (YIR013C)

PHO84 (YML123C)

KTR2 (YKR061W)

SJH1 (YIL002C)

Almost all of these also show a consistent dependency on STE7, STE7, and STE12. In tec1Δ, ste12Δ and ste7Δ ("down" mutants), expression of most of these genes were down-regulated by 1 to 1.5, 1.5 to 2, 2 to 2.5, 2.5 to 3 and greater than 3 fold. In contrast, in STE11-4 and TEC HC ("up" mutants), must of these genes were up-regulated by 1 to 1.5, 1.5 to 2, 2 to 2.5, 2.5 to 3, 3 to 3.5 and greater than 3.5 fold. One gene that was known previously to be regulated by the pathway, FLO11 (which encodes a cell surface protein required for pseudohyphal growth) is the second-most strongly regulated target. Detailed studies were performed on one of these targets, PGU1, which encodes a secreted carbohydrate-destroying enzyme. This enzyme breaks down a key component of plant cell walls, polygalacturonic acid (which is the main component of pectin).

Replace the paragraph at page 6, lines 12 through 18 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Remarkably, galacturonic acid, the breakdown product of pectin, causes the strong repression of a gene, TOT10/YEL033W, which is turned on in the filamentation MAPK pathway and which these results have shown is required for invasion and filamentation. Thus, work described herein has identified a new regulatory circuit in yeast in which a signal from the host feeds back on the filamentation/invasion pathway. This is the first demonstration of a specific interaction between yeast and its plant host. Figures [1-11] 1-9 show the data in detail.

Replace the paragraph at page 7, lines 6 through 16 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Accordingly, the invention relates to a method of inhibiting invasion of a host by a fungus, comprising contacting the fungus with a compound which inhibits expression of a gene expressed in the filamentation MAPK pathway [and which] that enhances the filamentation MAPK pathway, in sufficient quantity that inhibition of the expression of the gene occurs, thereby inhibiting invasion of the host by the fungus. In one embodiment, the host is a plant, and the compound is applied to a plant surface (e.g., a leaf, a root, a stem, a flower) in such a manner that it contacts the fungus. An effective amount of the compound can be determined empirically by assessing expression levels of

the gene to be inhibited. In a preferred embodiment, the gene is TOT10/YELO33W. In one embodiment, the fungus is a yeast, such as *Saccharomyces cerevisiae*.

Replace the paragraph at page 9, lines 13 through 22 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

The invention also relates to a method of identifying an agent which inhibits the filamentation MAPK pathway in a fungus, comprising the steps of providing an expression vector comprising a nucleic acid molecule of a gene which is expressed in the filamentation MAPK pathway; transforming a suitable host cell with said expression vector under conditions suitable for expression of said [gene] gene; contacting said host cell with an agent to be tested; and comparing the expression of said gene in the presence of the agent with the expression of said gene in the absence of said agent, wherein if the expression of said gene is lower in the presence of the agent than in the absence of the agent, then the agent is an inhibitor of the filamentation MAPK pathway in a fungus. In one embodiment, the gene is TOT10/YELO33W.

Replace the paragraph at page 10, lines 17 through 21 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

The invention further includes a method of inhibiting invasion of a host by a fungus, comprising contacting the fungus with a compound which enhances expression of a gene expressed in the filamentation MAPK pathway [and which] that inhibits the pathway, in sufficient quantity that enhancement of the expression of the gene occurs, thereby inhibiting invasion of the host by the fungus.

Claim Amendments Under 37 C.F.R. § 1.121(c)(1)(ii)

9. (Thrice Amended) A method of identifying an agent which inhibits the filamentation MAPK pathway in a fungus, comprising the steps of:

a) transforming a suitable host cell [capable of expressing a gene when transformed] with an expression vector comprising a nucleic acid molecule encoding TOT10/YEL033W under conditions suitable for expression of TOT10/YEL033W;

b) contacting said host cell with an agent to be tested; and

c) comparing the expression of TOT10/YEL033W in the presence of the agent with the expression of TOT10/YEL033W in the absence of said agent, wherein if the expression of TOT10/YEL033W is lower in the presence of the agent than in the absence of the agent, then the agent is an inhibitor of the filamentation MAPK pathway in a fungus.

15. (Thrice Amended) A method of identifying an agent which modulates PGUI gene expression, comprising the steps of:

a) transforming a suitable host cell [capable of expressing a gene when transformed] with an expression vector comprising a nucleic acid molecule encoding PGUI under conditions suitable for expression of PGUI;

b) contacting said host cell with an agent to be tested; and

c) comparing the expression of PGUI in the presence of the agent with the expression of PGUI in the absence of said agent, wherein a difference in the expression of PGUI in the presence of the agent as compared with in the absence of the agent indicates that the agent modulates PGUI expression.

19. (Twice Amended) A method of identifying an agent which modulates expression of a gene which is modulated by a filamentation MAPK pathway in a fungus, comprising the steps of:

a) transforming a suitable host cell [capable of expressing a gene when transformed] with an expression vector comprising a nucleic acid molecule encoding a gene selected from the group consisting of: PGU1, FLO11, TOT10/YEL033W, SRD1, TOT12/YKR105C, TOT13/YOR225W, FLO5, DDR48, TOT11/YLR042C, TOT7/YER158C, TOT8/YIL117C, TOT20/YHL049C, TOT15/YLR434C, TOT14/YBR113W, TOT9/YIR013C, PHO84, KTR2, and SJH1;

b) contacting said host cell with an agent to be tested; and

c) comparing the expression of said gene in the presence of the agent with the expression of said gene in the absence of said agent, wherein a difference in the expression of said gene in the presence of the agent as compared with in the absence of the agent indicates that the agent modulates expression of said gene which is modulated by the filamentation MAPK pathway in a fungus.

TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no, however, event will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G Leffers Jr. whose telephone number is (703) 308-6232. The examiner can normally be reached on 9:30am-6:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, George Elliot can be reached on (703) 308-4003. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 305-7939 for regular communications and (703) 305-7939 for After Final communications.

Any inquiry of a general nature or relating to the status of this application, or relating to attachments to this office action, should be directed to the Patent Analyst Zeta Adams, whose telephone number is (703) 305-3291.

Gerald G Leffers Jr.
Examiner
Art Unit 1636

GGL
Ggl
January 9, 2003

DAVID GUZO
PRIMARY EXAMINER